

1600

## RAW SEQUENCE LISTING

DATE: 10/23/2001

PATENT APPLICATION: US/09/555,342A

TIME: 10:57:38

Input Set : A:\so5025us.txt

Output Set: N:\CRF3\10232001\I555342A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
 5 <120> TITLE OF INVENTION: cDNA and deduced amino acid sequence in human fetus  
 chondrocytes  
 8 <130> FILE REFERENCE: CGS98-04PCT  
 10 <140> CURRENT APPLICATION NUMBER: US/09/555,342A  
 10 <141> CURRENT FILING DATE: 2000-05-26  
 10 <160> NUMBER OF SEQ ID NOS: 22  
 12 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

301 <210> SEQ ID NO: 2  
 302 <211> LENGTH: 1045  
 303 <212> TYPE: PRT  
 304 <213> ORGANISM: Homo sapiens  
 306 <400> SEQUENCE: 2  
 307 Met Gly Glu Ile Glu Gln Arg Pro Thr Pro Gly Ser Arg Leu Gly Ala  
 308 1 5 10 15  
 310 Pro Glu Asn Ser Gly Ile Ser Thr Leu Glu Arg Gly Gln Lys Pro Pro  
 311 20 25 30  
 313 Pro Thr Pro Ser Gly Lys Leu Val Ser Ile Lys Ile Gln Met Leu Asp  
 314 35 40 45  
 316 Asp Thr Gln Glu Ala Phe Glu Val Pro Gln Arg Ala Pro Gly Lys Val  
 317 50 55 60  
 319 Leu Leu Asp Ala Val Cys Asn His Leu Asn Leu Val Glu Gly Asp Tyr  
 320 65 70 75 80  
 322 Phe Gly Leu Glu Phe Pro Asp His Lys Lys Ile Thr Val Trp Leu Asp  
 323 85 90 95  
 325 Leu Leu Lys Pro Ile Val Lys Gln Ile Arg Arg Pro Lys His Val Val  
 326 100 105 110  
 328 Val Lys Phe Val Val Lys Phe Phe Pro Pro Asp His Thr Gln Leu Gln  
 329 115 120 125  
 331 Glu Glu Leu Thr Arg Tyr Leu Phe Ala Leu Gln Val Lys Gln Asp Leu  
 332 130 135 140  
 334 Ala Gln Gly Arg Leu Thr Cys Asn Asp Thr Ser Ala Ala Leu Leu Ile  
 335 145 150 155 160  
 337 Ser His Ile Val Gln Ser Glu Ile Gly Asp Phe Asp Glu Ala Leu Asp  
 338 165 170 175  
 340 Arg Glu His Leu Ala Lys Asn Lys Tyr Ile Pro Gln Gln Asp Ala Leu  
 341 180 185 190  
 343 Glu Asp Lys Ile Val Glu Phe His Asn His Ile Gly Gln Thr Pro  
 344 195 200 205  
 346 Ala Glu Ser Asp Phe Gln Leu Leu Glu Ile Ala Arg Arg Leu Glu Met  
 347 210 215 220  
 349 Tyr Gly Ile Arg Leu His Pro Ala Lys Asp Arg Glu Gly Thr Lys Ile  
 350 225 230 235 240  
 352 Asn Leu Ala Val Ala Asn Thr Gly Ile Leu Val Phe Gln Gly Phe Thr

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353          245          250          255
355 Lys Ile Asn Ala Phe Asn Trp Ala Lys Val Arg Lys Leu Ser Phe Lys
356          260          265          270
358 Arg Lys Arg Phe Leu Ile Lys Leu Arg Pro Asp Ala Asn Ser Ala Tyr
359          275          280          285
361 Gln Asp Thr Leu Glu Phe Leu Met Ala Ser Arg Asp Phe Cys Lys Ser
362          290          295          300
364 Phe Trp Lys Ile Cys Val Glu His His Ala Phe Phe Arg Leu Phe Glu
365 305          310          315          320
367 Glu Pro Lys Pro Lys Pro Lys Pro Val Leu Phe Ser Arg Gly Ser Ser
368          325          330          335
370 Phe Arg Phe Ser Gly Arg Thr Gln Lys Gln Val Leu Asp Tyr Val Lys
371          340          345          350
373 Glu Gly Gly His Lys Lys Val Gln Phe Glu Arg Lys His Ser Lys Ile
374          355          360          365
376 His Ser Ile Arg Ser Leu Ala Ser Gln Pro Thr Glu Leu Asn Ser Glu
377          370          375          380
379 Val Leu Glu Gln Ser Gln Gln Ser Thr Ser Leu Thr Phe Gly Glu Gly
380 385          390          395          400
382 Ala Glu Ser Pro Gly Gly Gln Ser Cys Arg Arg Gly Lys Glu Pro Lys
383          405          410          415
385 Val Ser Ala Gly Glu Pro Gly Ser His Pro Ser Pro Ala Pro Arg Arg
386          420          425          430
388 Ser Pro Ala Gly Asn Lys Gln Ala Asp Gly Ala Ala Ser Ala Pro Thr
389          435          440          445
391 Glu Glu Glu Glu Glu Val Val Lys Asp Arg Thr Gln Gln Ser Lys Pro
392          450          455          460
394 Gln Pro Pro Gln Pro Ser Thr Gly Ser Leu Thr Gly Ser Pro His Leu
395 465          470          475          480
397 Ser Glu Leu Ser Val Asn Ser Gln Gly Gly Val Ala Pro Ala Asn Val
398          485          490          495
400 Thr Leu Ser Pro Asn Leu Ser Pro Asp Thr Lys Gln Ala Ser Pro Leu
401          500          505          510
403 Ile Ser Pro Leu Leu Asn Asp Gln Ala Cys Pro Arg Thr Asp Asp Glu
404          515          520          525
406 Asp Glu Gly Arg Arg Lys Arg Phe Pro Thr Asp Lys Ala Tyr Phe Ile
407          530          535          540
409 Ala Lys Glu Val Ser Thr Thr Glu Arg Thr Tyr Leu Lys Asp Leu Glu
410 545          550          555          560
412 Val Ile Thr Ser Trp Phe Gln Ser Thr Val Ser Lys Glu Asp Ala Met
413          565          570          575
415 Pro Glu Ala Leu Lys Ser Leu Ile Phe Pro Asn Phe Glu Pro Leu His
416          580          585          590
418 Lys Phe His Thr Asn Phe Leu Lys Glu Ile Glu Gln Arg Leu Ala Leu
419          595          600          605
421 Trp Glu Gly Arg Ser Asn Ala Gln Ile Arg Asp Tyr Gln Arg Ile Gly
422          610          615          620
424 Asp Val Met Leu Lys Asn Ile Gln Gly Met Lys His Leu Ala Ala His
425 625          630          635          640

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```

427 Leu Trp Lys His Ser Glu Ala Leu Glu Ala Leu Glu Asn Gly Ile Lys
428                               645                               650                               655
430 Ser Ser Arg Arg Leu Glu Asn Phe Cys Arg Asp Phe Glu Leu Gln Lys
431                               660                               665                               670
433 Val Cys Tyr Leu Pro Leu Asn Thr Phe Leu Leu Arg Pro Leu His Arg
434                               675                               680                               685
436 Leu Met His Tyr Lys Gln Val Leu Glu Arg Leu Cys Lys His His Pro
437                               690                               695                               700
439 Pro Ser His Ala Asp Phe Arg Asp Cys Arg Ala Ala Leu Ala Glu Ile
440 705                               710                               715                               720
442 Thr Glu Met Val Ala Gln Leu His Gly Thr Met Ile Lys Met Glu Asn
443                               725                               730                               735
445 Phe Gln Lys Leu His Glu Leu Lys Lys Asp Leu Ile Gly Ile Asp Asn
446                               740                               745                               750
448 Leu Val Val Pro Gly Arg Glu Phe Ile Arg Leu Gly Ser Leu Ser Lys
449                               755                               760                               765
451 Leu Ser Gly Lys Gly Leu Gln Arg Met Phe Phe Leu Phe Asn Asp
452 770                               775                               780
454 Val Leu Leu Tyr Thr Ser Arg Gly Leu Thr Ala Ser Asn Gln Phe Lys
455 785                               790                               795                               800
457 Val His Gly Gln Leu Pro Leu Tyr Gly Met Thr Ile Glu Glu Ser Glu
458                               805                               810                               815
460 Asp Glu Trp Gly Val Pro His Cys Leu Thr Leu Arg Gly Gln Arg Gln
461                               820                               825                               830
463 Ser Ile Ile Val Ala Ala Ser Ser Arg Ser Glu Met Glu Lys Trp Val
464                               835                               840                               845
466 Glu Asp Ile Gln Met Ala Ile Asp Leu Ala Glu Lys Ser Ser Ser Pro
467 850                               855                               860
469 Ala Pro Glu Phe Leu Ala Ser Ser Pro Pro Asp Asn Lys Ser Pro Asp
470 865                               870                               875                               880
472 Glu Ala Thr Ala Ala Asp Gln Glu Ser Glu Asp Asp Leu Ser Ala Ser
473                               885                               890                               895
475 Arg Thr Ser Leu Glu Arg Gln Ala Pro His Arg Gly Asn Thr Met Val
476                               900                               905                               910
478 His Val Cys Trp His Arg Asn Thr Ser Val Ser Met Val Asp Phe Ser
479                               915                               920                               925
481 Ile Ala Val Glu Asn Gln Leu Ser Gly Asn Leu Leu Arg Lys Phe Lys
482 930                               935                               940
484 Asn Ser Asn Gly Trp Gln Lys Leu Trp Val Val Phe Thr Asn Phe Cys
485 945                               950                               955                               960
487 Leu Phe Phe Tyr Lys Ser His Gln Asp Asn His Pro Leu Ala Ser Leu
488                               965                               970                               975
490 Pro Leu Leu Gly Tyr Ser Leu Thr Ile Pro Ser Glu Ser Glu Asn Ile
491                               980                               985                               990
493 Gln Lys Asp Tyr Val Phe Lys Leu His Phe Lys Ser His Val Tyr Tyr
494                               995                               1000                               1005
496 Phe Arg Ala Glu Ser Glu Tyr Thr Phe Glu Arg Trp Met Glu Val Ile
497 1010                               1015                               1020
499 Arg Ser Ala Thr Ser Ser Ala Ser Arg Pro His Val Leu Ser His Lys

```

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E--> 500 025/025                      1030                      1035                      1040  
502 Glu Ser Leu Val Tyr  
503                      1045

## VERIFICATION SUMMARY

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Input Set : A:\so5025us.txt

Output Set: N:\CRF3\10232001\I555342A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:508 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:512 M:283 W: Missing Blank Line separator, <400> field identifier  
L:518 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:522 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
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L:542 M:283 W: Missing Blank Line separator, <400> field identifier  
L:548 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:552 M:283 W: Missing Blank Line separator, <400> field identifier  
L:558 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
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L:568 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
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